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OM protein - protein search, using sw model

Run on: May 7, 2002, 11:58:52 ; Search time 26.38 seconds
(without alignments)
190.229 Million cell updates/sec

Title: US-09-772-103-2

Perfect score: 1174

Sequence: 1 MACLGFORHKAQLNLRWTW.....MPTEPECEKQFQPYFTIPIN 223

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

al number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA.*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1158	98.6	223	3	US-08-228-208A-17
2	1103.5	94.0	234	1	US-08-505-058-1
3	1103.5	94.0	234	1	US-08-459-818-21
4	1103.5	94.0	234	2	US-08-889-666-21
5	1103.5	94.0	234	2	US-08-465-078-21
6	1103.5	94.0	234	2	US-08-725-776-21
7	1103.5	94.0	234	2	US-08-488-062-21
8	970	82.6	187	1	US-08-067-684-14
9	970	82.6	187	1	US-08-008-898-14
10	970	82.6	187	2	US-08-459-818-14
11	970	82.6	187	2	US-08-889-666-14
12	970	82.6	187	2	US-08-465-078-14
13	970	82.6	187	2	US-08-725-776-14
14	970	82.6	187	3	US-08-488-062-14
15	970	82.6	187	3	US-08-228-208A-14
16	967	82.4	187	5	PCT-US95-06726-36
17	857	73.0	223	3	US-08-228-208A-18
18	804.5	68.5	234	1	US-08-505-058-2
19	804.5	68.5	234	2	US-08-459-818-22
20	804.5	68.5	234	2	US-08-889-666-22
21	804.5	68.5	234	2	US-08-465-078-22
22	804.5	68.5	234	2	US-08-725-776-22
23	804.5	68.5	234	2	US-08-488-062-22
24	648	55.2	124	3	US-08-630-172-4
25	648	55.2	124	4	US-09-375-419-4
26	648	55.2	357	3	US-08-630-172-20
27	648	55.2	357	4	US-09-375-419-20

ALIGNMENTS

RESULT 1
US-08-228-208A-17
; Sequence 17, Application US/08228208A
; Patent No. 6090914
; GENERAL INFORMATION:
; APPLICANT: Linsley, Peter S.
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Damle, Nitin K.
; APPLICANT: Brady, William
; APPLICANT: Wallace, Philip M.
; TITLE OF INVENTION: CTLA4/CD28Tg HYBRID FUSION
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 11150 Santa Monica Boulevard, Suite 400
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/228,208A
; FILING DATE: 15-APR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/008,898
; FILING DATE: 22-JAN-1993
; APPLICATION NUMBER: 07/723,617
; FILING DATE: 27-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Adriano, Sarah B.
; REGISTRATION NUMBER: 34,470
; REFERENCE/DOCKET NUMBER: 30436-30US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310 445-1140
; TELEFAX: 310 445-9031
; TELEX:
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 223 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-228-208A-17

Sequence 20, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 2, Appl
Sequence 4, Appl
Sequence 6, Appl
Sequence 26, Appl
Sequence 26, Appl
Sequence 26, Appl
Sequence 26, Appl

QY 1 MACLGFORHKAQLNLAATRTWPCITLLFLLFIPVFCAMHVAQPAVVLASSRGIAFVCEY 60
Db 1 MACLGFORHKAQLNLAATRTWPCITLLFLLFIPVFCAMHVAQPAVVLASSRGIAFVCEY 60
QY 61 ASPGKATEVRVTVLRQADSOVTEVCAATYMMGNELTFLDSDS--ICTGTSSGNQVNLTIQG 118
Db 61 ASPGKATEVRVTVLRQADSOVTEVCAATYMMGNELTFLDSDSXXICTGTSSGNQVNLTIQG 120
QY 119 LRAMDTGLYICKVELMYPYPYLL--GIGNGAQIYVIDPEPC-----PDSDFLLWILAIVSS 172
Db 121 LRAMDTGLYICKVELMYPYPYLLXGIGNGTQIYVIDPEPCXXXPDSDDFLLWILAIVSS 180
QY 173 GLFFYSFLLT-AVSLSKMLKKRSPLTGTVVYVKNPPTPEPECE--KQFQYFIPIN 223
Db 181 GLFFYSFLLTAVSLSKMLKKRSPLTGTVVYVKNPPTPEPECEXXKQFQYFIPIN 234

RESULT 3
US-08-459-818-21
; Sequence 21, Application US/08459818
; Patent No. 5851795
; GENERAL INFORMATION:
; APPLICANT: Linsley, Peter S.
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Damle, Nitin K.
; APPLICANT: Brady, William
; TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Merchant & Gould
; STREET: 11150 Santa Monica Blvd., Suite 400
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90025

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FastSeq 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,818
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Adriano, Sarah B.
REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 30436.35US02
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-445-1140
TELEFAX: 310-445-9031
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 234 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-818-21

Query Match 94.0%; Score 1103.5; DB 2; Length 234;
Best Local Similarity 94.0%; Pred. No. 1.4e-105;
Matches 220; Conservative 0; Mismatches 3; Indels 11; Gaps 5;

QY 1 MACLGFORHKAQLNLAATRTWPCITLLFLLFIPVFCAMHVAQPAVVLASSRGIAFVCEY 60
Db 1 MACLGFORHKAQLNLAATRTWPCITLLFLLFIPVFCAMHVAQPAVVLASSRGIAFVCEY 60
QY 61 ASPGKATEVRVTVLRQADSOVTEVCAATYMMGNELTFLDSDS--ICTGTSSGNQVNLTIQG 118
Db 61 ASPGKATEVRVTVLRQADSOVTEVCAATYMMGNELTFLDSDSXXICTGTSSGNQVNLTIQG 120

Query Match 98.6%; Score 1158; DB 3; Length 223;
Best Local Similarity 98.7%; Pred. No. 3.4e-111;
Matches 220; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 MACLGFORHKAQLNLAATRTWPCITLLFLLFIPVFCAMHVAQPAVVLASSRGIAFVCEY 60
Db 1 MACLGFORHKAQLNLAATRTWPCITLLFLLFIPVFCAMHVAQPAVVLASSRGIAFVCEY 60
QY 61 ASPGKATEVRVTVLRQADSOVTEVCAATYMMGNELTFLDSDSICTGTSSGNQVNLTIQGLR 120
Db 61 ASPGKATEVRVTVLRQADSOVTEVCAATYMMGNELTFLDSDSICTGTSSGNQVNLTIQGLR 120
QY 121 AMDTGLYICKVELMYPYPYLLGIGNGAQIYVIDPEPCPSDSDFLWILAIVSSGLFFYSFL 180
Db 121 AMDTGLYICKVELMYPYPYLLGIGNGTQIYVIDPEPCPSDSDFLWILAIVSSGLFFYSFL 180
QY 181 LTAVSLSKMLKKRSPLTGTVVYVKNPPTPEPECEKQFQYFIPIN 223
Db 181 LTAVSLSKMLKKRSPLTGTVVYVKNPPTPEPECEKQFQYFIPIN 223

RESULT 2
US-08-505-058-1
; Sequence 1, Application US/08505058
; Patent No. 5773253
; GENERAL INFORMATION:
; APPLICANT: Linsley, Peter S.
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Peach, Robert
; TITLE OF INVENTION: CTLA4 Mutant Molecules and Uses Thereof
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Merchant & Gould
; STREET: 11150 Santa Monica Blvd., Suite 400
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90025

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/505,058
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/228,208
FILING DATE: 15-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Adriano, Sarah B.
REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 30436.3005I1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-445-1140
TELEFAX: 310-445-9031
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 234 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-505-058-1

Query Match 94.0%; Score 1103.5; DB 1; Length 234;
Best Local Similarity 94.0%; Pred. No. 1.4e-105;
Matches 220; Conservative 0; Mismatches 3; Indels 11; Gaps 5;

QY 1 MACLGFORHKAQLNLAATRTWPCITLLFLLFIPVFCAMHVAQPAVVLASSRGIAFVCEY 60
Db 1 MACLGFORHKAQLNLAATRTWPCITLLFLLFIPVFCAMHVAQPAVVLASSRGIAFVCEY 60
QY 61 ASPGKATEVRVTVLRQADSOVTEVCAATYMMGNELTFLDSDS--ICTGTSSGNQVNLTIQG 118
Db 61 ASPGKATEVRVTVLRQADSOVTEVCAATYMMGNELTFLDSDSXXICTGTSSGNQVNLTIQG 120

QY 119 LRAMDTGLYICKVELMPPPPYL-GINGAQIYVIDPEPC-----PDSDFLLWILAASS 172
Db 121 LRAMDTGLYICKVELMPPPPYLXGIGNGTQIYVIDPEPCXXXXXPSDFLLWILAASS 180
QY 173 GLFFYSFLLT-AVSLSKMLKKRSPLTTGVYVKMPPTPECE--KQFPYFIPIN 223
Db 181 GLFFYSFLLT-XAVSLSKMLKKRSPLTTGVYVKMPPTPECEXXKQFPYFIPIN 234

RESULT 4
US-08-889-666-21
; Sequence 21, Application US/08889666
; Patent No. 5885579
; GENERAL INFORMATION:
; APPLICANT: Linsley, Peter S.
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Damle, Nitin K.
; APPLICANT: Brady, William
; APPLICANT: Kiener, Peter A.
; TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 11150 Santa Monica Blvd., Suite 400
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90025

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/889,666
FILING DATE: 08-JUL-1997
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/375390
FILING DATE: 18-JAN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Adriano, Sarah B.
REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 30436-35US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-445-1140
TELEFAX: 310-445-9031

INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 234 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-889-666-21

Query Match 94.0%; Score 1103.5; DB 2; Length 234;
Best Local Similarity 94.0%; Pred. No. 1.4e-105;
Matches 220; Conservative 0; Mismatches 3; Indels 11; Gaps 5;

QY 1 MACLGFORHKAQLNATRTWPTCTLLFFLLFIPVFCAMHVAQPAVVLASSRGIAFVCEY 60
Db 1 MACLGFORHKAQLNATRTWPTCTLLFFLLFIPVFCAMHVAQPAVVLASSRGIAFVCEY 60
QY 61 ASPGKATEVRVTVLRQADSOVTEVCAATYMGNETLFLDSDSXXICTGSSGNQVNLTIQ 118
Db 61 ASPGKATEVRVTVLRQADSOVTEVCAATYMGNETLFLDSDSXXICTGSSGNQVNLTIQ 120
QY 119 LRAMDTGLYICKVELMPPPPYL-GINGAQIYVIDPEPC-----PDSDFLLWILAASS 172
Db 121 LRAMDTGLYICKVELMPPPPYLXGIGNGTQIYVIDPEPCXXXXXPSDFLLWILAASS 180

QY 173 GLFFYSFLLT-AVSLSKMLKKRSPLTTGVYVKMPPTPECE--KQFPYFIPIN 223
Db 181 GLFFYSFLLT-XAVSLSKMLKKRSPLTTGVYVKMPPTPECEXXKQFPYFIPIN 234

RESULT 5
US-08-465-078-21
; Sequence 21, Application US/08465078
; Patent No. 5885796
; GENERAL INFORMATION:
; APPLICANT: Linsley, Peter S.
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Damle, Nitin K.
; APPLICANT: Brady, William
; APPLICANT: Kiener, Peter A.
; TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 11150 Santa Monica Blvd., Suite 400
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90025

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,078
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/375390
FILING DATE: 18-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Adriano, Sarah B.
REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 30436-35US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-445-1140
TELEFAX: 310-445-9031

INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 234 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-465-078-21

Query Match 94.0%; Score 1103.5; DB 2; Length 234;
Best Local Similarity 94.0%; Pred. No. 1.4e-105;
Matches 220; Conservative 0; Mismatches 3; Indels 11; Gaps 5;

QY 1 MACLGFORHKAQLNATRTWPTCTLLFFLLFIPVFCAMHVAQPAVVLASSRGIAFVCEY 60
Db 1 MACLGFORHKAQLNATRTWPTCTLLFFLLFIPVFCAMHVAQPAVVLASSRGIAFVCEY 60
QY 61 ASPGKATEVRVTVLRQADSOVTEVCAATYMGNETLFLDSDSXXICTGSSGNQVNLTIQ 118
Db 61 ASPGKATEVRVTVLRQADSOVTEVCAATYMGNETLFLDSDSXXICTGSSGNQVNLTIQ 120
QY 119 LRAMDTGLYICKVELMPPPPYL-GINGAQIYVIDPEPC-----PDSDFLLWILAASS 172
Db 121 LRAMDTGLYICKVELMPPPPYLXGIGNGTQIYVIDPEPCXXXXXPSDFLLWILAASS 180
QY 173 GLFFYSFLLT-AVSLSKMLKKRSPLTTGVYVKMPPTPECE--KQFPYFIPIN 223
Db 181 GLFFYSFLLT-XAVSLSKMLKKRSPLTTGVYVKMPPTPECEXXKQFPYFIPIN 234

us-09-772-103-2.rai

Mon Jul 1 16:28:06 2002

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; Sequence 21, Application US/08488062
; Patent No. 5977318
; GENERAL INFORMATION:
; APPLICANT: Linsley, Peter S.
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Damle, Nitin K.
; APPLICANT: Brady, William
; APPLICANT: Kiener, Peter A.
; TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 11150 Santa Monica Blvd., Suite 400
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,062
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/375390
; FILING DATE: 18-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Adriano, Sarah B.
; REGISTRATION NUMBER: 34,470
; REFERENCE/DOCKET NUMBER: 30436-35US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-445-1140
; TELEFAX: 310-445-9031
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 234 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-488-062-21

Query Match      94.0%; Score 1103.5; DB 2; Length 234;
Best Local Similarity 94.0%; Pred. No. 1.4e-105;
Matches 220; Conservative 0; Mismatches 3; Indels 11; Gaps 5;

QY 1 MACLGFORHKAQLNLAATRTWPCITLLFFLLFIPVFCAMHVAQPAVVLAASSRGIAFVCEY 60
Db 1 MACLGFORHKAQLNLAARTWPCITLLFFLLFIPVFCAMHVAQPAVVLAASSRGIAFVCEY 60
QY 61 ASPGKATEVRVTVLRLQADSQVTEVCAATYMGNELTFLDSDS--ICTGTSSGNQVNLTIQG 118
Db 61 ASPGKATEVRVTVLRLQADSQVTEVCAATYMGNELTFLDSDSXXICTGTSSGNQVNLTIQG 120
QY 119 LRAMDTGLYICKVELMYPPIYL-GTNGAQIYVIDPEPC-----PDSDFLLWILAASS 172
Db 121 LRAMDTGLYICKVELMYPPIYLGGTNGAQIYVIDPEPCXXXXPDSDFLLWILAASS 180
QY 173 GLFFYSFLLT-AVSLSKMLKRSPLTTGVVVKMPPTPEPE--KQFPYFIPIN 223
Db 181 GLFFYSFLLTAVSLSKMLKRSPLTTGVVVKMPPTPEPECEXXKQFPYFIPIN 234

RESULT 8
US-08-067-684-14
; Sequence 14, Application US/08067684
; Patent No. 5434131
; GENERAL INFORMATION:
; APPLICANT: Linsley, Peter S.
; Sequence 21, Application US/08488062
; Patent No. 5977318
; GENERAL INFORMATION:
; APPLICANT: Linsley, Peter S.
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Damle, Nitin K.
; APPLICANT: Brady, William
; APPLICANT: Kiener, Peter A.
; TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 11150 Santa Monica Blvd., Suite 400
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/725,776
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/375390
; FILING DATE: 18-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Adriano, Sarah B.
; REGISTRATION NUMBER: 34,470
; REFERENCE/DOCKET NUMBER: 30436-35US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-445-1140
; TELEFAX: 310-445-9031
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 234 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-725-776-21

Query Match      94.0%; Score 1103.5; DB 2; Length 234;
Best Local Similarity 94.0%; Pred. No. 1.4e-105;
Matches 220; Conservative 0; Mismatches 3; Indels 11; Gaps 5;

QY 1 MACLGFORHKAQLNLAATRTWPCITLLFFLLFIPVFCAMHVAQPAVVLAASSRGIAFVCEY 60
Db 1 MACLGFORHKAQLNLAARTWPCITLLFFLLFIPVFCAMHVAQPAVVLAASSRGIAFVCEY 60
QY 61 ASPGKATEVRVTVLRLQADSQVTEVCAATYMGNELTFLDSDS--ICTGTSSGNQVNLTIQG 118
Db 61 ASPGKATEVRVTVLRLQADSQVTEVCAATYMGNELTFLDSDSXXICTGTSSGNQVNLTIQG 120
QY 119 LRAMDTGLYICKVELMYPPIYL-GTNGAQIYVIDPEPC-----PDSDFLLWILAASS 172
Db 121 LRAMDTGLYICKVELMYPPIYLGGTNGAQIYVIDPEPCXXXXPDSDFLLWILAASS 180
QY 173 GLFFYSFLLT-AVSLSKMLKRSPLTTGVVVKMPPTPEPE--KQFPYFIPIN 223
Db 181 GLFFYSFLLTAVSLSKMLKRSPLTTGVVVKMPPTPEPECEXXKQFPYFIPIN 234

RESULT 7
US-08-488-062-21
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;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: FastSeq 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/459,818
;; FILING DATE: 02-JUN-1995
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Adriano, Sarah B.
;; REGISTRATION NUMBER: 34,470
;; REFERENCE/DOCKET NUMBER: 30436.35US02
;; TELEPHONE: 310-445-1140
;; TELEFAX: 310-445-9031
;; INFORMATION FOR SEQ ID NO: 14:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 187 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-889-818-14

Query Match 82.6%; Score 970; DB 2; Length 187;
Best Local Similarity 99.5%; Pred. No. 5.1e-92;
Matches 186; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 37 AMHVAQPAVVLASSRGIAFVCEYASPGKATEVRVTVLRQADSQVTEVCAATYMMGNELT 96
DB 1 AMHVAQPAVVLASSRGIAFVCEYASPGKATEVRVTVLRQADSQVTEVCAATYMMGNELT 60

QY 97 FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMPPPPYVLGIGNGAQIYVIDPEP 156
DB 61 FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMPPPPYVLGIGNGAQIYVIDPEP 120

QY 157 CPDSDFLWLILAAVSSGLFFYSFLLTAVSLSKMLKRSPLTTGVYVKKMPPTPECEKQFQ 216
DB 121 CPDSDFLWLILAAVSSGLFFYSFLLTAVSLSKMLKRSPLTTGVYVKKMPPTPECEKQFQ 180

QY 217 PYFIPIN 223
DB 181 PYFIPIN 187

RESULT 12
US-08-465-078-14
; Sequence 14, Application US/08465078
; Patent No. 5885796
; GENERAL INFORMATION:
; APPLICANT: Linsley, Peter S.
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Damle, Nitin K.
; APPLICANT: Brady, William
; APPLICANT: Kienert, Peter A.
; TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 11150 Santa Monica Blvd., Suite 400
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,078
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER: US 08/375390
; FILING DATE: 18-JAN-1995
; ATTORNEY/AGENT INFORMATION:

;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: FastSeq 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/459,818
;; FILING DATE: 02-JUN-1995
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Adriano, Sarah B.
;; REGISTRATION NUMBER: 34,470
;; REFERENCE/DOCKET NUMBER: 30436.35US02
;; TELEPHONE: 310-445-1140
;; TELEFAX: 310-445-9031
;; INFORMATION FOR SEQ ID NO: 14:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 187 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-889-818-14

Query Match 82.6%; Score 970; DB 2; Length 187;
Best Local Similarity 99.5%; Pred. No. 5.1e-92;
Matches 186; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 37 AMHVAQPAVVLASSRGIAFVCEYASPGKATEVRVTVLRQADSQVTEVCAATYMMGNELT 96
DB 1 AMHVAQPAVVLASSRGIAFVCEYASPGKATEVRVTVLRQADSQVTEVCAATYMMGNELT 60

QY 97 FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMPPPPYVLGIGNGAQIYVIDPEP 156
DB 61 FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMPPPPYVLGIGNGAQIYVIDPEP 120

QY 157 CPDSDFLWLILAAVSSGLFFYSFLLTAVSLSKMLKRSPLTTGVYVKKMPPTPECEKQFQ 216
DB 121 CPDSDFLWLILAAVSSGLFFYSFLLTAVSLSKMLKRSPLTTGVYVKKMPPTPECEKQFQ 180

QY 217 PYFIPIN 223
DB 181 PYFIPIN 187

RESULT 11
US-08-889-666-14
; Sequence 14, Application US/08889666
; Patent No. 5885579
; GENERAL INFORMATION:
; APPLICANT: Linsley, Peter S.
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Damle, Nitin K.
; APPLICANT: Brady, William
; APPLICANT: Kienert, Peter A.
; TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 11150 Santa Monica Blvd., Suite 400
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/889,666
; FILING DATE: 08-JUL-1997
; CLASSIFICATION: 435

NAME: Adriano, Sarah B.
REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 30436-35US01
TELEPHONE: 310-445-1140
TELEFAX: 310-445-9031
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 187 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-465-078-14

Query Match 82.6%; Score 970; DB 2; Length 187;
Best Local Similarity 99.5%; Pred. No. 5.1e-92;
Matches 186; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

37 AMHVAQPAVVLAASSRGIAFVCEYASPGKATEVRVTVLRLQADSOQVTEVCAATYMMGNELT 96
1 AMHVAQPAVVLAASSRGIAFVCEYASPGKATEVRVTVLRLQADSOQVTEVCAATYMMGNELT 60
97 FLDDSTCTGTSSGNQVNLTIQGLRAMDTGLYICKVELMPPPPYVVGNGAQIYVIDPEP 156
61 FLDDSTCTGTSSGNQVNLTIQGLRAMDTGLYICKVELMPPPPYVVGNGAQIYVIDPEP 120
97 CPDSDFLWILAAVSSGLFFYSFLLTAVSLSKMLKRSPLTTGVVVKMPPTPECEKQFQ 216
121 CPDSDFLWILAAVSSGLFFYSFLLTAVSLSKMLKRSPLTTGVVVKMPPTPECEKQFQ 180
217 PYFIPIN 223
181 PYFIPIN 187

RESULT 13
US-08-725-776-14
Sequence 14, Application US/08725776
Patent No. 5968510

GENERAL INFORMATION:
APPLICANT: Linsley, Peter S.
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Damle, Nitin K.
APPLICANT: Brady, William
APPLICANT: Kiener, Peter A.
TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 11150 Santa Monica Blvd., Suite 400
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90025

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/725,776
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/375390
FILING DATE: 18-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Adriano, Sarah B.
REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 30436-35US01
TELEPHONE: 310-445-1140

TELEFAX: 310-445-9031
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 187 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-725-776-14

Query Match 82.6%; Score 970; DB 2; Length 187;
Best Local Similarity 99.5%; Pred. No. 5.1e-92;
Matches 186; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

37 AMHVAQPAVVLAASSRGIAFVCEYASPGKATEVRVTVLRLQADSOQVTEVCAATYMMGNELT 96
1 AMHVAQPAVVLAASSRGIAFVCEYASPGKATEVRVTVLRLQADSOQVTEVCAATYMMGNELT 60
97 FLDDSTCTGTSSGNQVNLTIQGLRAMDTGLYICKVELMPPPPYVVGNGAQIYVIDPEP 156
61 FLDDSTCTGTSSGNQVNLTIQGLRAMDTGLYICKVELMPPPPYVVGNGAQIYVIDPEP 120
97 CPDSDFLWILAAVSSGLFFYSFLLTAVSLSKMLKRSPLTTGVVVKMPPTPECEKQFQ 216
121 CPDSDFLWILAAVSSGLFFYSFLLTAVSLSKMLKRSPLTTGVVVKMPPTPECEKQFQ 180
217 PYFIPIN 223
181 PYFIPIN 187

RESULT 14
US-08-488-062-14
Sequence 14, Application US/08488062
Patent No. 5977318

GENERAL INFORMATION:
APPLICANT: Linsley, Peter S.
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Damle, Nitin K.
APPLICANT: Brady, William
APPLICANT: Kiener, Peter A.
TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 11150 Santa Monica Blvd., Suite 400
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90025

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,062
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/375390
FILING DATE: 18-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Adriano, Sarah B.
REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 30436-35US01
TELEPHONE: 310-445-1140
TELEFAX: 310-445-9031
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 187 amino acids
TYPE: amino acid

MOLECULE TYPE: protein
US-08-228-208A-14

Query Match 82.6%; Score 970; DB 3; Length 187;
Best Local Similarity 99.5%; Pred. No. 5.1e-92; Indels 0; Gaps 0;
Matches 186; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 37 AMHVAQPAVVLASSRGIAFVCEYASPGKATEVRVTVLRQADSQVTEVCAATYMMGNELT 96
Db 1 AMHVAQPAVVLASSRGIAFVCEYASPGKATEVRVTVLRQADSQVTEVCAATYMMGNELT 60
QY 97 FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMYPYPYLGIGNGAQIYVIDPEP 156
Db 61 FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMYPYPYLGIGNGAQIYVIDPEP 120
QY 157 CPDSDFLWLTLAAVSSGLFFYSFLLTAVSLSKMLKKRSPLTTGVYVVKMPPTPECEKQFQ 216
Db 121 CPDSDFLWLTLAAVSSGLFFYSFLLTAVSLSKMLKKRSPLTTGVYVVKMPPTPECEKQFQ 180
QY 217 PYFIPIN 223
Db 181 PYFIPIN 187

Search completed: May 7, 2002, 12:01:21
Job time: 149 sec

MOLECULE TYPE: protein
US-08-488-062-14

Query Match 82.6%; Score 970; DB 2; Length 187;
Best Local Similarity 99.5%; Pred. No. 5.1e-92; Indels 0; Gaps 0;
Matches 186; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 37 AMHVAQPAVVLASSRGIAFVCEYASPGKATEVRVTVLRQADSQVTEVCAATYMMGNELT 96
Db 1 AMHVAQPAVVLASSRGIAFVCEYASPGKATEVRVTVLRQADSQVTEVCAATYMMGNELT 60
QY 97 FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMYPYPYLGIGNGAQIYVIDPEP 156
Db 61 FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMYPYPYLGIGNGAQIYVIDPEP 120
QY 157 CPDSDFLWLTLAAVSSGLFFYSFLLTAVSLSKMLKKRSPLTTGVYVVKMPPTPECEKQFQ 216
Db 121 CPDSDFLWLTLAAVSSGLFFYSFLLTAVSLSKMLKKRSPLTTGVYVVKMPPTPECEKQFQ 180
QY 217 PYFIPIN 223
Db 181 PYFIPIN 187

RESULT 15
US-08-228-208A-14
Sequence 14, Application US/08228208A
Patent No. 6090914
GENERAL INFORMATION:
APPLICANT: Lionsley, Peter S.
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Damle, Nitin K.
APPLICANT: Brady, William
APPLICANT: Wallace, Philip M.
TITLE OF INVENTION: CTLA4/CD28lg HYBRID FUSION
TITLE OF INVENTION: PROTEINS AND USES THEREOF
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 11150 Santa Monica Boulevard, Suite 400
CITY: Los Angeles
STATE: CA
COUNTRY: USA
ZIP: 90025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/228,208A
FILING DATE: 15-APR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/008,898
FILING DATE: 22-JAN-1993
APPLICATION NUMBER: 07/723,617
FILING DATE: 27-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Adriano, Sarah B
REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 30436-30US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310 445-1140
TELEFAX: 310 445-9031
TELEX:
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 187 amino acids
TYPE: amino acid
TOPOLOGY: linear

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 7, 2002, 11:59:17 ; Search time 32.09 Seconds
(without alignments)
529.353 Million cell updates/sec

Title: US-09-772-103-2
Perfect score: 1174
Sequence: 1 MACLGFORHKAQLNLAIRTW.....MPPTPECEKQFPYFIPIN 223

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues
Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1159	98.7	223	2 T09536	cytotoxic T-lympho
2	997	84.9	223	2 I46696	CTLA-4 precursor
3	970	82.6	186	2 S08614	cytotoxic T-lympho
4	878	74.8	223	2 A29063	cytotoxic T-lympho
5	211	18.0	221	2 S25168	CD28 protein - ch
6	204	17.4	221	2 I46689	CD28 precursor - r
7	200	17.0	36	2 I84732	cytotoxic T-lympho
8	187	15.9	220	1 RWHU28	T-cell surface gly
9	174.5	14.9	173	2 I46197	cell surface prote
10	170	14.5	218	2 A43523	T-cell surface gly
11	158	13.5	218	2 S24413	T-cell surface gly
12	101	8.6	132	2 S38646	Ig kappa chain V r
13	100.5	8.6	120	2 S46370	Ig kappa chain V-J
14	99	8.4	124	2 S40336	Ig kappa chain V-J
15	97	8.3	108	2 S30521	Ig kappa chain V r
16	97	8.3	128	2 S46372	Ig kappa chain var
17	94	8.0	117	2 S46371	Ig kappa chain V r
18	93	7.9	132	2 S40334	Ig kappa chain V-J
19	92	7.8	117	2 S41812	Ig kappa chain V-J
20	91	7.8	108	2 S34007	Ig kappa chain V r
21	91	7.8	4391	2 A38096	Ig kappa chain V r
22	90.5	7.7	108	2 S36277	perlecan precursor
23	90.5	7.7	123	2 S40378	Ig lambda chain V
24	90	7.7	140	2 PL0013	Ig kappa chain - h
25	89.5	7.6	3707	2 S18252	Ig kappa chain pre
26	89	7.6	125	2 S40353	heparan sulfate pr
27	88	7.5	573	2 S12838	Ig kappa chain V-J
28	87.5	7.5	88	2 S34104	Ig mu chain precu
29	87.5	7.5	213	2 A21177	Ig kappa chain V r
					Ig light chain pre

30 87 7.4 207 2 I50609 T-cell surface gly
31 87 7.4 739 2 J50675 vascular cell adhe
32 86 7.3 120 2 S30525 Ig lambda chain V
33 86 7.3 125 2 S40349 Ig kappa chain V-J
34 86 7.3 199 2 S78540 inducible T-cell c
35 86 7.3 234 2 S14237 Ig kappa chain pre
36 86 7.3 739 2 JN0581 vascular cell adhe
37 85.5 7.3 598 2 T42070 protein serine/thr
38 85 7.2 111 2 S36281 Ig lambda chain V
39 85 7.2 112 2 PL0274 Ig kappa chain V r
40 85 7.2 125 2 S40333 Ig kappa chain V-J
41 85 7.2 1367 2 A41228 protein-tyrosine k
42 84.5 7.2 105 2 S26338 Ig kappa chain V r
43 84.5 7.2 124 2 S40318 Ig kappa chain V r
44 84 7.2 111 2 S38497 Ig lambda chain -
45 84 7.2 112 2 H26317 Ig kappa chain V r

ALIGNMENTS

RESULT 1
T09536
cytotoxic T-lymphocyte protein 4 - human
C:Species: Homo sapiens (man)
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C:Accession: T09536
R:Harper, K.; Balzano, C.; Rouvier, E.; Mattei, M.G.; Luciani, M.F.; Golstein, P.
J. Immunol. 147, 1037-1044, 1991
A:Title: CTLA-4 and CD28 activated lymphocyte molecules are closely related in both m
A:Reference number: I49584; MOID:91318145
A:Accession: T09536
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-223 <HAR>
A:Cross-references: EMBL:L15006; NID:g291928; PIDN:AAB59385.1; PID:g291929
C:Genetics:
A:Gene: CTLA4
A:Map position: 2q33
C:Superfamily: T-cell surface glycoprotein CD28; immunoglobulin homology
C:Keywords: T-cell; transmembrane protein

Query Match 98.7%; Score 1159; DB 2; Length 223;
Best Local Similarity 98.7%; Pred. No. 4.6e-100;
Matches 220; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 MACLGFORHKAQLNLAIRTWPCITLLFFLIPVFCAMHVAQPAVVLASSRGIAFVCEY 60
Db 1 MACLGFORHKAQLNLAIRTWPCITLLFFLIPVFCAMHVAQPAVVLASSRGIAFVCEY 60
Qy 61 ASPGKATEVRYTVLRQADSOVTEVCAATYMMGNELTFDDSDICTCTSSGNQVNLTIQGLR 120
Db 61 ASPGKATEVRYTVLRQADSOVTEVCAATYMMGNELTFDDSDICTCTSSGNQVNLTIQGLR 120
Qy 121 AMDTGLYICKVELMYPPIYIGNGAIYVIDPECPDSDFLWLILAAVSSGLFFYSFL 180
Db 121 AMDTGLYICKVELMYPPIYIGNGAIYVIDPECPDSDFLWLILAAVSSGLFFYSFL 180
Qy 181 LTAVSLSKMLKKRPLTGTGVYVKMPPTPECEKQFPYFIPIN 223
Db 181 LTAVSLSKMLKKRPLTGTGVYVKMPPTPECEKQFPYFIPIN 223

RESULT 2
I46696
CTLA-4 precursor - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 05-Nov-1999
C:Accession: I46696
R:Isono, T.; Seto, A.
Immunogenetics 42, 217-220, 1995
A:Title: Cloning and sequencing of the rabbit gene encoding T-cell costimulatory mole

A:Reference number: I46689; MUID:95369849
A:Accession: I46696
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-223 <ISO>
A:Cross-references: GB:D49844; NID:g755100; PIDN:BAA08644.1; PID:g755101
C:Superfamily: T-cell surface glycoprotein CD28; immunoglobulin homology

Query Match 84.9%; Score 997; DB 2; Length 223;
Best Local Similarity 84.3%; Pred. No. 4.7e-85;
Matches 188; Conservative 16; Mismatches 19; Indels 0; Gaps 0;

QY 1 MACIGFORHKAQLNLAIRTPWCTLLFLLFIPVFCAMHVAQPAVVLASSRGIAFVCEY 60
DB 1 MARLGFORQGTQLDLASRTWSCAALFLLFIPVFSKALHVSQPAVVLASSRGVAFVCEY 60

QY 61 ASPGKATEVRVTVLROADSQVTEVCAATYMMGNELFLDSDICTGSSGNQVNLTIQGLR 120
DB 61 ASSHKATEVRVTVLROADSQVTEVCAATYMMGNELFLDSDICTGSSGNQVNLTIQGLR 120

QY 121 AMDTGLYICKVELMYPYPYVILGNGAQIYVIDPEPCDSDFLWLAASVSSGLFFYSFL 180
DB 121 AMDTGLYICKVELMYPYPYVILGNGAQIYVIDPEPCDSDFLWLAASVSSGLFFYSFL 180

QY 181 LTAVSLSKMLKKRSLPTGTGVYVVKMPPECEKQFQYFIPIN 223
DB 181 ITAVSLSKMLKKRSLPTGTGVYVVKMPPECEKQFQYFIPIN 223

RESULT 3
S08614
cytotoxic T-lymphocyte protein 4 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 11-Jan-2000
R:Accession: S08614
R:Dariavach, P.; Mattei, M.G.; Golstein, P.; Lefranc, M.P.
Eur. J. Immunol. 18, 1901-1905, 1988
A:Title: Human Ig superfamily CTLA-4 gene: chromosomal localization and identity of pro
A:Reference number: S08614; MUID:89120925
A:Accession: S08614
A:Molecule type: DNA
A:Residues: 1-186 <DAR>
A:Cross-references: EMBL:X15070; NID:g30283; PID:g825649
C:Genetics:
A:Gene: GDB:CTLA4
A:Cross-references: GDB:119818; OMIM:123890
Map position: 2q33-2q33
Superfamily: T-cell surface glycoprotein CD28; immunoglobulin homology
C:Keywords: transmembrane protein
F:125-150/Domain: transmembrane #status predicted <TM>
F:151-186/Domain: intracellular #status predicted <INT>
F:21-92/disulfide bonds: #status predicted

Db 181 YFIPIN 186
|||||
RESULT 4
A29063
cytotoxic T-lymphocyte protein 4 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change 05-Nov-1999
A:Accession: A29063; I49622
R:Brune, J.F.; Denizot, F.; Luciani, M.F.; Roux-Dosseto, M.; Suzan, M.; Mattei, M.G.
Nature 328, 267-270, 1987
A:Title: A new member of the immunoglobulin superfamily--CTLA-4.
A:Reference number: A29063; MUID:87258259
A:Accession: A29063
A:Molecule type: mRNA
A:Residues: 1-223

A:Cross-references: GB:X05719; NID:g50592; PIDN:CAA29191.1; PID:g50593
R:Harper, K.; Balzano, C.; Rouvier, E.; Mattei, M.G.; Luciani, M.F.; Golstein, P.
J. Immunol. 147, 1037-1044, 1991
A:Title: CTLA-4 and CD28 activated lymphocyte molecules are closely related in both m
A:Reference number: I49584; MUID:91318145
A:Accession: I49622
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-36 <RES>
A:Cross-references: GB:M74362; NID:g192833; PIDN:AAA37489.1; PID:g553903
C:Genetics:
A:Gene: CtlA-4
A:Map position: 1, band C
C:Superfamily: T-cell surface glycoprotein CD28; immunoglobulin homology
C:Keywords: transmembrane protein

Query Match 74.8%; Score 878; DB 2; Length 223;
Best Local Similarity 74.0%; Pred. No. 5e-74;
Matches 165; Conservative 23; Mismatches 35; Indels 0; Gaps 0;

QY 1 MACIGFORHKAQLNLAIRTPWCTLLFLLFIPVFCAMHVAQPAVVLASSRGIAFVCEY 60
DB 1 MACIGLRRYKAQLPSRTPWFVALLTLFIPVFSRAIQVTPSVVLASSHGVAFFCEY 60

QY 61 ASPGKATEVRVTVLROADSQVTEVCAATYMMGNELFLDSDICTGSSGNQVNLTIQGLR 120
DB 61 SPSHNTDEVRTVLRTQNDQMTVECATTTTEKNTVGLDYPPFCSGTFNESRVNLTIQGLR 120

QY 121 AMDTGLYICKVELMYPYPYVILGNGAQIYVIDPEPCDSDFLWLAASVSSGLFFYSFL 180
DB 121 AVDTGLYICKVELMYPYPYVILGNGAQIYVIDPEPCDSDFLWLAASVSSGLFFYSFL 180

QY 181 LTAVSLSKMLKKRSLPTGTGVYVVKMPPECEKQFQYFIPIN 223
DB 181 VSAVSLSKMLKKRSLPTGTGVYVVKMPPECEKQFQYFIPIN 223

RESULT 5
S25168
CHT28 protein - chicken
C:Species: Gallus gallus (chicken)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
A:Accession: I50619; S25168
R:Young, J.R.; Davison, T.F.; Tregaskes, C.A.; Rennie, M.C.; Vainio, O.
J. Immunol. 152, 3848-3851, 1994
A:Title: Monomeric homologue of mammalian CD28 is expressed on chicken T cells.
A:Reference number: I50619; MUID:94194147
A:Accession: I50619
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-221 <Y02>
A:Cross-references: EMBL:X67915; NID:g63221; PIDN:CAA48114.1; PID:g63222
C:Superfamily: T-cell surface glycoprotein CD28; immunoglobulin homology
C:Keywords: transmembrane protein

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OM protein - protein search, using sw model

Run on: May 7, 2002, 12:01:22 ; Search time 19.81 Seconds
(without alignments)
412.734 Million cell updates/sec

Title: US-09-772-103-2

Perfect score: 1174

Sequence: 1 MACLGFORHKAQLNLAIRTW.....MPTEPCERKQFQPIPIPIN 223

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1174	100.0	223	1	CTLA_HUMAN
2	1010	86.0	223	1	CTLA_PIG
3	997	84.9	223	1	CTLA_RABIT
4	878	74.8	223	1	CTLA_MOUSE
5	211	18.0	221	1	CD28_CHICK
6	204	17.4	221	1	CD28_RABIT
7	203	17.3	219	1	CD28_BOVIN
8	187	15.9	220	1	CD28_HUMAN
9	170	14.5	218	1	CD28_MOUSE
10	156	13.3	218	1	CD28_RAT
11	91	7.8	4393	1	PGBM_HUMAN
12	89.5	7.6	3707	1	PGBM_MOUSE
13	87	7.4	739	1	VCAL_RAT
14	86	7.3	739	1	VCAL_MOUSE
15	85	7.2	1356	1	VGR2_HUMAN
16	85	7.2	1367	1	VGR2_MOUSE
17	83	7.1	111	1	LV2A_HUMAN
18	83	7.1	111	1	LV2D_HUMAN
19	83	7.1	1343	1	VGR2_RAT
20	82	7.0	215	1	CTB2_HUMAN
21	81.5	6.9	111	1	KV12_RABIT
22	81.5	6.9	1897	1	PTF_HUMAN
23	81	6.9	246	1	MOG_MOUSE
24	79.5	6.8	108	1	KV6K_MOUSE
25	79	6.7	550	1	VGLE_HSVEL
26	78.5	6.7	108	1	KV1H_HUMAN
27	78.5	6.7	108	1	OPCM_RAT
28	78.5	6.7	345	1	OPCM_HUMAN
29	78	6.6	485	1	SAHH_MESCR
30	78	6.6	3038	1	TRIO_HUMAN
31	77.5	6.6	226	1	C79A_HUMAN
32	77.5	6.6	345	1	OPCM_BOVIN
33	77.5	6.6	345	1	OPCM_HUMAN

RESULT	1	CTLA_HUMAN	STANDARD	PRT	223 AA
AC	P16410				
DT	01-AUG-1990 (Rel. 15, Created)				
DT	01-APR-1993 (Rel. 25, Last sequence update)				
DT	20-AUG-2001 (Rel. 40, Last annotation update)				
DE	CYTOTOXIC T-LYMPHOCYTE PROTEIN 4 PRECURSOR (CYTOTOXIC T-LYMPHOCYTE-ASSOCIATED ANTIGEN 4) (CTLA-4) (CD152 ANTIGEN).				
GN	CTLA4 OR CD152.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_Taxid:9606;				
RN	[1]				
RP	SEQUENCE OF 1-37 FROM N.A.				
RX	MEDLINE=91318145; PubMed=1713603;				
RA	Harper K., Balzano C., Rouvier E., Mattei M.-G., Luciani M.F.,				
RA	Golstein P.;				
RT	"CTLA-4 and CD28 activated lymphocyte molecules are closely related				
RT	in both mouse and human as to sequence, message expression, gene				
RT	structure, and chromosomal location.";				
RL	J. Immunol. 147:1037-1044(1991).				
RN	[2]				
RP	SEQUENCE OF 38-223 FROM N.A.				
RC	TISSUE=Lymphocytes;				
RX	MEDLINE=89120525; PubMed=3220103;				
RA	Darlavach P., Mattei M.-G., Golstein P., Lefranc M.-P.;				
RT	"Human Ig superfamily CTLA-4 gene: chromosomal localization and				
RT	identity of protein sequence between murine and human CTLA-4				
RT	cytoplasmic domains.";				
RL	Eur. J. Immunol. 18:1901-1905(1988).				
RN	[3]				
RP	FUNCTION.				
RX	MEDLINE=91341416; PubMed=1714933;				
RA	Linsley P.S., Brady W., Unes M., Griensmaire L.S., Damle N.K.,				
RA	Ledbetter J.A.;				
RT	"CTLA-4 is a second receptor for the B cell activation antigen B7.";				
RL	J. Exp. Med. 174:561-569(1991).				
RN	[4]				
RP	STRUCTURE BY NMR OF 37-165				
RX	MEDLINE=97372889; PubMed=9228944;				
RA	Metzler W.J., Bajorath J., Fenderson W., Shaw S.Y., Constantine K.L.,				
RA	Naemura J., Leytze G., Peach R.J., Lavoie T.B., Mueller L.,				
RA	Linsley P.S.;				
RT	"Solution structure of human CTLA-4 and delineation of a CD80/CD86				
RT	binding site conserved in CD28.";				
RL	Nat. Struct. Biol. 4:527-531(1997).				
CC	-I- FUNCTION: POSSIBLY INVOLVED IN T-CELL ACTIVATION. BINDS TO B7-1				
CC	(CD80) AND B7-2 (CD86).				
CC	-I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.				
CC	-I- TISSUE SPECIFICITY: CELL SURFACE OF ACTIVATED T-LYMPHOCYTES.				
CC	-I- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.				
CC	-I- DATABASE: NAME=PROW; NOTE=CD guide CD152 entry;				
CC	WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd152.htm".				

ALIGNMENTS

34	77	6.6	109	1	KV01_RAT
35	76.5	6.5	129	1	KV3M_HUMAN
36	76.5	6.5	1203	1	PTC2_HUMAN
37	76	6.5	109	1	LV2E_HUMAN
38	76	6.5	114	1	KV4A_HUMAN
39	76	6.5	3562	1	PGCV_CHICK
40	75.5	6.4	108	1	KVIG_HUMAN
41	75.5	6.4	149	1	KV5A_MOUSE
42	75.5	6.4	485	1	SAHH_WHEAT
43	75	6.4	112	1	KV2D_MOUSE
44	75	6.4	115	1	KV3I_HUMAN
45	75	6.4	117	1	KV1J_HUMAN

P01681 rattus norv
P18136 homo sapien
Q996C5 homo sapien
P01708 homo sapien
P01625 homo sapien
Q90953 gallus gall
P01599 homo sapien
P01633 mus musculu
P32112 triticum ae
P01629 mus musculu
P04433 homo sapien
P01602 homo sapien

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CC -----
CC EMBL; M74363; AAA52127.1; -
CC EMBL; M37245; AAA52773.1; -
CC EMBL; M37243; AAA52773.1; JOINED.
CC EMBL; M37244; AAA52773.1; JOINED.
CC PIR; S08614; S08614.
CC PDB; 1AH1; 15-APR-98.
CC MIM; 123890; -
CC InterPro: IPR003596; Ig_v.
CC SMART; SM00406; IGV; 1.
CC Immunoglobulin domain; T-cell; Transmembrane; Glycoprotein; Signal;
KW 3D-structure.

CC SIGNAL 1 35
CC CHAIN 36 223
CC DOMAIN 36 161
CC TRANSMEM 162 187
CC DOMAIN 188 223
CC DOMAIN 39 140
CC DISULFID 58 129
CC DISULFID 85 103
CC CARBOHYD 113 113
CC SEQUENCE 223 AA; 24626 MW; 7525D6FB3E029B4A CRC64;
Query Match 100.0%; Score 1174; DB 1; Length 223;
Best Local Similarity 100.0%; Pred. No. 8.9e-102; Indels 0; Gaps 0;
Matches 223; Conservative 0; Mismatches 0;
QY 1 MACLGFORHKAQLNATRTWPCITLLFLLFIPVFCAMHVAQPAVVLASSRGIAFVCEY 60
DB 1 MACLGFORHKAQLNATRTWPCITLLFLLFIPVFCAMHVAQPAVVLASSRGIAFVCEY 60
QY 61 ASPGKATEVRVTVLRQADSOQTEVCAATYMMGNELTFLDSDICTGTSGNOVNLTIOGLR 120
DB 61 ASPGKATEVRVTVLRQADSOQTEVCAATYMMGNELTFLDSDICTGTSGNOVNLTIOGLR 120
QY 121 AMDTGLYICKVELMPPPPYLYGIGNGAQIYVIDPEPCPSDFLLWILAAVSSGLFFYSFL 180
DB 121 AMDTGLYICKVELMPPPPYLYGIGNGAQIYVIDPEPCPSDFLLWILAAVSSGLFFYSFL 180
QY 181 LTAVSLSKMLKKRSLPTTGVYVVKMPPTPECEKQFQYFIPIN 223
DB 181 LTAVSLSKMLKKRSLPTTGVYVVKMPPTPECEKQFQYFIPIN 223

RESULT 2
CTLA_PIG STANDARD; PRT; 223 AA.
ID CTLA_PIG
AC Q9MYX7;
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE CYTOTOXIC T-LYMPHOCYTE PROTEIN 4 PRECURSOR (CYTOTOXIC T-LYMPHOCYTE-
DE ASSOCIATED ANTIGEN 4) (CTLA-4).
GN CTLA4.
OS Sus scrofa (Pig).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Tachdjian M., Chaplin P.J., Scheerlinck J.-P.Y., Tennent J.M.;
RT "Molecular characterization and phylogenetic analysis of porcine
RT cytotoxic T-lymphocyte-associated antigen 4 (CTLA4).";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: POSSIBLY INVOLVED IN T-CELL ACTIVATION. BINDS TO B7-1

CC (CD80) AND B7-2 (CD86) (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF281633; AAF86981.1; -
CC InterPro: IPR003599; Ig.
CC InterPro: IPR003006; Ig_MHC.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00409; IGV; 1.
CC Immunoglobulin domain; T-cell; Transmembrane; Glycoprotein; Signal.
KW SIGNAL 1 35
CC CHAIN 36 223
CC DOMAIN 36 161
CC TRANSMEM 162 187
CC DOMAIN 188 223
CC DOMAIN 39 140
CC DISULFID 58 129
CC DISULFID 85 103
CC CARBOHYD 113 113
CC CARBOHYD 145 145
CC SEQUENCE 223 AA; 24430 MW; 2DD865D871D8921 CRC64;
Query Match 86.0%; Score 1010; DB 1; Length 223;
Best Local Similarity 85.2%; Pred. No. 1.4e-86;
Matches 190; Conservative 14; Mismatches 19; Indels 0; Gaps 0;

QY 1 MACLGFORHKAQLNATRTWPCITLLFLLFIPVFCAMHVAQPAVVLASSRGIAFVCEY 60
DB 1 MACSGFQSHGAWLELTSRTWPCITLLFLLFIPVFCAMHVAQPAVVLASSRGIAFVCEY 60
QY 61 ASPGKATEVRVTVLRQADSOQTEVCAATYMMGNELTFLDSDICTGTSGNOVNLTIOGLR 120
DB 61 ASPGKATEVRVTVLRQADSOQTEVCAATYMMGNELTFLDSDICTGTSGNOVNLTIOGLR 120
QY 121 AMDTGLYICKVELMPPPPYLYGIGNGAQIYVIDPEPCPSDFLLWILAAVSSGLFFYSFL 180
DB 121 AMDTGLYICKVELMPPPPYLYGIGNGAQIYVIDPEPCPSDFLLWILAAVSSGLFFYSFL 180
QY 181 LTAVSLSKMLKKRSLPTTGVYVVKMPPTPECEKQFQYFIPIN 223
DB 181 LTAVSLSKMLKKRSLPTTGVYVVKMPPTPECEKQFQYFIPIN 223

RESULT 3
CTLA_RABIT STANDARD; PRT; 223 AA.
ID CTLA_RABIT
AC P42072;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE CYTOTOXIC T-LYMPHOCYTE PROTEIN 4 PRECURSOR (CYTOTOXIC T-LYMPHOCYTE-
DE ASSOCIATED ANTIGEN 4) (CTLA-4).
GN CTLA4.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=B/J X CHBB:HM;
RX MEDLINE=95369849; PubMed=7642234;
RA Isono T., Seto A.;
RT "Cloning and sequencing of the rabbit gene encoding T-cell
RT costimulatory molecules.";
RT

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OM protein - protein search, using sw model

Run on: May 7, 2002, 12:00:52 ; Search time 54.19 Seconds
(without alignments)
601.933 Million cell updates/sec

Title: US-09-772-103-2

Perfect score: 1174

Sequence: 1 MACLGQRHKAQLNLAIRTW.....MPTEPCERKQFQYFIPIN 223

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_17:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1122	95.6	223	6	Q9BDN7 papio anubi
2	1118	95.2	223	6	Q9BDC4 macaca mulla
3	1076	91.7	223	6	Q9BDP1 aotus trivi
4	1034	88.1	223	6	Q9XTA1 felis silve
5	1032	87.9	223	6	Q9FT02 canis fami
6	1022	87.1	223	6	Q9GKP2 canis fami
7	1014	86.4	223	6	Q9XSY7 felis silve
8	1006	85.7	223	6	Q9N186 sus scrofa
9	997	84.9	223	6	Q9XS11 canis fami
10	996	84.8	223	11	Q9JLV3 marmota mon
11	984	83.8	221	6	Q28090 bos taurus
12	975	83.0	221	6	Q97631 ovine aries
13	896	76.3	223	11	Q62859 ratius norv
14	882	75.1	223	11	Q9QZ27 mus musculu
15	592	50.4	137	4	Q95653 homo sapien
16	587	50.0	115	4	Q9BZK2 homo sapien
17	534	45.5	174	11	Q9Z1A7 rattus norv
18	442	37.6	84	4	Q9UKN9 homo sapien
19	252	21.5	68	11	Q99PF8 cricetus

20	199.5	17.0	221	6	Q9GKP3 canis fami
21	198	16.9	219	6	Q97630 ovine aries
22	196.5	16.7	221	6	Q9N0N8 canis fami
23	191.5	16.3	221	6	Q02757 felis silve
24	190.5	16.2	221	6	Q9N214 felis silve
25	189	16.1	220	6	Q9BDN2 callithrix
26	188.5	16.1	220	6	Q9BDN8 papio anubi
27	187.5	16.0	220	6	Q9BDM8 macaca neme
28	186.5	15.9	220	6	Q9BDN5 macaca mulla
29	185.5	15.8	221	11	Q9JLV4 marmota mon
30	178.5	15.2	220	6	Q9BDM6 macaca mulla
31	174.5	14.9	173	6	Q28289 canis fami
32	113.5	9.7	201	4	Q14931 homo sapien
33	110	9.4	176	4	Q95667 homo sapien
34	108	9.2	44	11	Q9Z1A8 mus musculu
35	107	9.1	177	4	Q14930 homo sapien
36	107	9.1	190	4	Q14932 homo sapien
37	103.5	8.8	152	4	Q95668 homo sapien
38	103.5	8.8	165	4	Q95669 homo sapien
39	97	8.3	269	4	Q95297 homo sapien
40	96	8.2	108	4	Q9UL79 homo sapien
41	94.5	8.0	243	4	Q9DEL4 homo sapien
42	94	8.0	209	4	Q9NYK4 homo sapien
43	91.5	7.8	183	4	Q9UEL6 homo sapien
44	91.5	7.8	235	11	Q99M11 mus musculu
45	91	7.8	4370	4	Q9H3V5 homo sapien

ALIGNMENTS

RESULT 1

Q9BDN7 ID Q9BDN7 PRELIMINARY; PRT; 223 AA.
AC Q9BDN7;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE C0152 PROTEIN PRECURSOR.
GN CTIA-4.
OS Papio anubis (Olive baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheciae; Papio.
OX NCBI_Taxid=9555;
RN [1]
RP SEQUENCE FROM N.A.
RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
RA Weiss W.R., Ansari A.A.;
RT "Cloning, sequencing and homology analysis of nonhuman primate
RT Fas/Fas-Ligand and co-stimulatory molecules.";
RL Immunogenetics 0:0-0(2001).
DR EMBL; AF344838; AAK37534.1; -.
KW Signal.
FT SIGNAL
SQ SEQUENCE 223 AA; 24655 MW; EC18C279CCCC5668 CRC64;

Query Match 95.6%; Score 1122; DB 6; Length 223;
Best Local Similarity 96.9%; Pred. No. 4.6e-99;
Matches 216; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY	1	MACLGQRHKAQLNLAIRTWPCITLLFELFPECKAMHVAQPAVVLASSRGTSFVCEY	60
DB	1	MACLGQRHKAQLNLAIRTPYLLFSLFIPVFSKAMHVAQPAVVLANSRGTSFVCEY	60
QY	61	ASPGKATEVRVTVLRQADSQVTEVCAATYMGNELFLDSDICTGTSSGNQVNLTIQGLR	120
DB	61	ASPGKATEVRVTVLRQADSQVTEVCAATYMGNELFLDSDICTGTSSGNQVNLTIQGLR	120
QY	121	AMDTGLYICKVELMYPYPPYLLGNGAQIYVIDPECPDSDFLWLTLAAVSSGLFFYSFL	180
DB	121	AMDTGLYICKVELMYPYPPYLLGNGAQIYVIDPECPDSDFLWLTLAAVSSGLFFYSFL	180

0000

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OM protein - protein search, using sw model

Run on: May 7, 2002, 11:58:42 ; Search time 53.91 Seconds
(without alignments)
306.406 Million cell updates/sec

Title: US-09-772-103-2

Perfect score: 1174

Sequence: 1 MACLGQRHKAQLNLATRTW.....MPTEPECEKQFPYFIPIN 223

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

al number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_1101.*

1:	/SID88/gcgdata/geneseq/geneseq/AA1980.DAT.*
2:	/SID88/gcgdata/geneseq/geneseq/AA1981.DAT.*
3:	/SID88/gcgdata/geneseq/geneseq/AA1982.DAT.*
4:	/SID88/gcgdata/geneseq/geneseq/AA1983.DAT.*
5:	/SID88/gcgdata/geneseq/geneseq/AA1984.DAT.*
6:	/SID88/gcgdata/geneseq/geneseq/AA1985.DAT.*
7:	/SID88/gcgdata/geneseq/geneseq/AA1986.DAT.*
8:	/SID88/gcgdata/geneseq/geneseq/AA1987.DAT.*
9:	/SID88/gcgdata/geneseq/geneseq/AA1988.DAT.*
10:	/SID88/gcgdata/geneseq/geneseq/AA1989.DAT.*
11:	/SID88/gcgdata/geneseq/geneseq/AA1990.DAT.*
12:	/SID88/gcgdata/geneseq/geneseq/AA1991.DAT.*
13:	/SID88/gcgdata/geneseq/geneseq/AA1992.DAT.*
14:	/SID88/gcgdata/geneseq/geneseq/AA1993.DAT.*
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16:	/SID88/gcgdata/geneseq/geneseq/AA1995.DAT.*
17:	/SID88/gcgdata/geneseq/geneseq/AA1996.DAT.*
18:	/SID88/gcgdata/geneseq/geneseq/AA1997.DAT.*
19:	/SID88/gcgdata/geneseq/geneseq/AA1998.DAT.*
20:	/SID88/gcgdata/geneseq/geneseq/AA1999.DAT.*
21:	/SID88/gcgdata/geneseq/geneseq/AA2000.DAT.*
22:	/SID88/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1174	100.0	223	22	Human CTLA4.
2	1170	99.7	223	21	Human CTLA-4 prote
3	1159	98.7	223	18	Soluble human CTLA
4	1159	98.7	223	22	Human CTLA4 protei
5	1103.5	94.0	234	20	Human CTLA4 protei
6	1034	88.1	223	20	Feline CTLA4 prote
7	1022	87.1	223	20	Canine CTLA4 prote
8	1015	86.5	223	21	Feline CTLA-4. Fe
9	1015	86.5	223	21	Cat CTLA-4 recepto
10	1006	85.7	223	21	Porcine CTLA-4 sol
11	984.5	83.9	211	20	Human CTLA4 recept

12	983	83.7	212	15	AAR60134	CTLA4 receptor fus
13	983	83.7	212	16	AAR77642	Full length CTLA4
14	983	83.7	212	20	AAW43479	Amino acid sequenc
15	983	83.7	212	20	AAW81584	Human CTLA4 recept
16	979	83.4	212	14	AAR31040	Human CTLA4 recept
17	977	83.2	223	22	AAU00686	Porcine CTLA4 prot
18	970	82.6	187	20	AAU41130	CTLA4 receptor wit
19	970	82.6	187	20	AAW97615	Human CTLA recepto
20	970	82.6	187	20	AAW97610	Human CTLA recepto
21	967	82.4	187	17	AAW86945	Human T cell speci
22	957	81.5	187	19	AAW29728	Soluble CTLA4 muta
23	837	71.3	168	19	AAW42340	CTLA-4 extracellul
24	804.5	68.5	234	20	AAW41134	Mouse CTLA4 protei
25	686	58.4	400	21	AAW15123	Porcine CTLA-4-Ig
26	672	57.2	364	21	AAW93698	Fusion protein of
27	667.5	56.9	377	18	AAW26208	CTLA4-modified IgG
28	667	56.8	374	18	AAW26206	CTLA4-IgG4 fusion
29	667	56.8	374	18	AAW26207	CTLA4-modified IgG
30	658	56.0	260	22	AAU00685	Human CTLA4-human
31	648	55.2	124	18	AAW35847	Human CTLA4 for us
32	648	55.2	357	18	AAW35863	Human CTLA4:IgG2a
33	642	54.7	357	19	AAW68134	Amino acid sequenc
34	642	54.7	470	19	AAW68135	Amino acid sequenc
35	638.5	54.4	253	20	AAW41132	CTLA4/E7 fusion pr
36	638.5	54.4	253	20	AAW43480	Amino acid sequenc
37	638.5	54.4	253	20	AAW1502	Amino terminal CTL
38	638.5	54.4	253	20	AAW97612	Amino terminal CTL
39	638.5	54.4	253	20	AAW87562	CTLA4-E7 fusion pr
40	638.5	54.4	253	20	AAW81586	CTLA4/E7 fusion pr
41	638.5	54.4	502	20	AAW41131	CTLA4/p97 fusion p
42	638.5	54.4	502	20	AAW43605	Amino acid sequenc
43	638.5	54.4	502	20	AAW97616	Amino terminal CTL
44	638.5	54.4	502	20	AAW97611	Amino terminal CTL
45	638.5	54.4	502	20	AAW87561	CTLA4-p97 fusion p

ALIGNMENTS

RESULT 1

AAAG66519	standard; Protein; 223 AA.
AC	AAAG66519;
DT	22-OCT-2001 (first entry)
XX	Human CTLA4.
XX	Human; CTLA4; cytotoxic T lymphocyte associated antigen 4; anti-CTLA4;
KW	immunosuppressive; immunomodulator; antiallergic; vaccine; antibody;
KW	T cell; humanised antibody; autoimmune disorder; graft rejection;
KW	allergy.
XX	Homo sapiens.
XX	WO200154732-A1.
PN	02-AUG-2001.
PD	26-JAN-2001; 2001WO-US02653.
XX	27-JAN-2000; 2000US-0178473.
XX	(GEM) GENETICS INST INC.
PI	Carreno BM, Wood C, Turner K, Collins M, Gray GS, Morris D;
PI	O'Hara D, Hinton P, Tsurushita N;
XX	WPI; 2001-483195/52.
DR	N-PSDB; AAH76437.
XX	Novel antibody-toxic group conjugate comprising an antibody that

PT recognizes a molecule expressed only on activated T cells, useful for
 PT modulating immune response for treating autoimmune disorder, allergic
 XX response -

Example 3; Page 114-115; 123pp; English.

XX The invention relates to an antibody-toxic group conjugate comprising
 CC an antibody that specifically recognises a molecule expressed only on
 CC activated T cells, and a toxic group. The T cell molecule is
 CC preferably human cytotoxic T lymphocyte associated antigen 4 (CTLA4).
 CC The antibody of the invention is a humanised anti-CTLA4 antibody
 CC comprising a sequence of 128 or 142 amino acids fully defined in the
 CC specification. The antibody-toxic group conjugate is useful for
 CC modulating the immune response in a subject suffering from a disorder
 CC or condition such as autoimmune disorder, immune response to a graft,
 CC allergic response or an immune response to a therapeutic protein.
 CC The antibody is also useful for research purposes, e.g., in staining
 CC and isolating CTLA4-bearing cells. The antibody is also useful for
 CC T-cell typing, for isolating specific IL-2 receptor-bearing cells or
 CC fragments of the receptor, for vaccine preparation, and for determining
 CC the effectiveness of an agent to down-regulate CTLA4 activity. The
 CC present sequence is human CTLA4, which is bound by the antibody
 CC provided in the invention.

XX Sequence 223 AA;

Query Match 100.0%; Score 1174; DB 22; Length 223;
 Best Local Similarity 100.0%; Pred. No. 3e-106;
 Matches 223; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MACIGFORHKAQLNLTATRWPTCTLLFFLLFPVCKAMHVAQPAVLASSRGIAFVCEY 60
 DB 1 macigfgrhkaqlnltatrwptctllffllfpvckamhvaqpavlassrgiasfvcey 60
 QY 61 ASPGKATEVRVTVLRLQADSQVTEVCAATYMMGNELTFLLDSDICTGSSGNOVNLTIOGLR 120
 DB 61 aspgkatevrvtvlrlqadsqvtevcattymmgneftfllddsictgssgnqvnltioglrl 120
 QY 121 AMDTGLYCKVELMYPPIYIGNGAQIYVIDPEPCDPSDFLLWILAASVSGLFFYSFL 180
 DB 121 amdgtglyckvelmypyppyyigngaqiyvidpepcpsdfllwilaavssgglffysfl 180
 QY 181 LTAVSLSKMLKKRSLPTGTGVYVKMPPTPECEKQFPYFIPIN 223
 DB 181 ltavslskmlkkrslptgtgvvkmppptecekekqfpyfipin 223

RESULT 2
 AAW25129 standard; protein; 223 AA.

XX AC AAV15129;
 XX DT 07-FEB-2000 (first entry)
 XX DE Human CTLA-4 protein.
 XX KW Human CTLA-4; soluble protein; xenograft; organ transplant; B7; CD28;
 KW xenograft-specific immunosuppression; recipient T-cell; anergy;
 KW co-stimulatory signal 2; homology; porcine CTLA-4.

XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 XX FT Peptide 1..37
 XX FT /label= Signal_peptide

XX W09957266-A2.
 XX 11-NOV-1999.
 XX 30-APR-1959; 99WO-GB01350.

XX 30-APR-1998; 98GB-0009280.
 XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
 XX PI Lechler IR, Dorling A;

XX WPI; 2000-038815/03.
 XX N-PSDB; AAZ29001.
 XX Inhibiting T-cell mediated rejection of xenotransplanted organs
 XX Disclosure; Fig 15; 43pp; English.

XX The present sequence is the human CTLA-4 soluble protein for
 CC xenograft-specific immunosuppression. Soluble CTLA-4 when administered to
 CC the organ recipient preferentially binds B7 on the xenograft and blocks
 CC its interaction with CD28 on recipient T-cells. The delivery of co
 CC stimulatory signal 2 is blocked and the T-cells are rendered anergic.
 CC This sequence has an overall homology of 85.2% with porcine CTLA-4 DNA.

XX Sequence 223 AA;

Query Match 99.7%; Score 1170; DB 21; Length 223;
 Best Local Similarity 99.6%; Pred. No. 7.4e-106;
 Matches 222; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MACIGFORHKAQLNLTATRWPTCTLLFFLLFPVCKAMHVAQPAVLASSRGIAFVCEY 60
 DB 1 macigfgrhkaqlnltatrwptctllffllfpvckamhvaqpavlassrgiasfvcey 60
 QY 61 ASPGKATEVRVTVLRLQADSQVTEVCAATYMMGNELTFLLDSDICTGSSGNOVNLTIOGLR 120
 DB 61 aspgkatevrvtvlrlqadsqvtevcattymmgneftfllddsictgssgnqvnltioglrl 120
 QY 121 AMDTGLYCKVELMYPPIYIGNGAQIYVIDPEPCDPSDFLLWILAASVSGLFFYSFL 180
 DB 121 amdgtglyckvelmypyppyyigngaqiyvidpepcpsdfllwilaavssgglffysfl 180
 QY 181 LTAVSLSKMLKKRSLPTGTGVYVKMPPTPECEKQFPYFIPIN 223
 DB 181 ltavslskmlkkrslptgtgvvkmppptecekekqfpyfipin 223

RESULT 3
 AAW25111 standard; protein; 223 AA.

XX AC AAW25111;
 XX DT 03-NOV-1997 (first entry)
 XX DE Soluble human CTLA4 mutant molecule reactive with CD80 antigen.
 XX KW CTLA4; mutant; soluble; CD80 antigen; specific; immune system;
 KW T cell surface receptor; B7-1; antibody production inhibitor; allergy;
 KW autoimmune disease; chronic inflammation; allograft rejection;
 KW graft versus host disease.

XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 XX FT Peptide 1..37
 XX FT /label= sig_peptide
 XX FT Protein 38..234
 XX FT /label= mat_protein
 XX FT Region 62..67
 XX FT /note= "CDR 1-like region"
 XX FT Region 86..90
 XX FT /note= "CDR 2-like region"
 XX FT Region 132..139
 XX FT /note= "CDR 3-like region; highly conserved"